

<!--StartFragment-->RESULT 4

AAQ28389
 ID AAQ28389 standard; DNA; 2907 BP.
 XX
 AC AAQ28389;
 XX
 DT 27-AUG-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 12-FEB-1993 (first entry)
 XX
 DE Gene from the ALS mutant of *Arabidopsis*.
 XX
 KW Herbicide resistant; acetolactate synthase; ALS; sulphonylurea;
 KW triazolopyrimidinesulphonamide; imidazolinone; markers; ss.
 XX
 OS *Arabidopsis thaliana*.
 XX
 FH Key Location/Qualifiers
 FT CDS 506..2518
 FT /*tag= a
 XX
 PN US5141870-A.
 XX
 PD 25-AUG-1992.
 XX
 PF 18-JAN-1991; 91US-00642976.
 XX
 PR 26-AUG-1986; 86US-00900609.
 PR 04-MAR-1988; 88US-00164360.
 XX
 PA (DUP0) DU PONT DE NEMOURS & CO E I.
 XX
 PI Bedbrook JR, Chaleff RS, Falco SC, Mazur BJ, Somerville CR;
 PI Yadav NS;
 XX
 DR WPI; 1992-307863/37.
 DR P-PSDB; AAR26913.
 XX
 PT Conferring herbicide resistance on plants - using a nucleic acid fragment
 PT encoding a herbicide-resistant plant aceto:lactate synthase protein.
 XX
 PS Disclosure; Fig 10; 63pp; English.
 XX
 CC The DNA sequence is that of a mutant acetolactate synthetase gene
 CC isolated from herbicide resistant strains of *Arabidopsis thaliana*.
 CC designated GH50. The GH50 mutant ALS gene may be isolated from
 CC *Arabidopsis* plants resistant to sulphonylurea, triazolopyrimidine
 CC sulphonamide and imidazolinone herbicides. The gene may be used to
 CC transform plants to confer herbicide resistance to plants such as
 CC tobacco, petunia, cotton, sugarbeet, potato, tomato, lettuce, sunflower,
 CC soybean, corn, wheat, rice, poplars, alfalfa, oats, etc. The herbicide
 CC resistant ALS genes can also be used as markers for transformation of an
 CC organism by a second DNA fragment. See also AAQ28387-8. (Updated on 25-
 CC MAR-2003 to correct PF field.) (Updated on 27-AUG-2003 to correct OS
 CC field.)
 XX
 SQ Sequence 2907 BP; 757 A; 610 C; 636 G; 904 T; 0 U; 0 Other;

Query Match 50.8%; Score 2903.8; DB 2; Length 2907;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 2905; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	1979	GCTCTTAGTTGTTATTGTTTGTAGCCAAATTCTCATTCTTATTCCATTTCACCTT	2038
Db	1	GCTCTTAGTTGTTATTGTTTGTAGCCAAATTCTCATTCTTATTCCATTTCACCTT	60
Qy	2039	ATCTCTGTTCTTATAGACCTTATAAGTTTTATTCTATGTATACAAATTATATTGTCA	2098
Db	61	ATCTCTGTTCTTATAGACCTTATAAGTTTTATTCTATGTATACAAATTATATTGTCA	120
Qy	2099	TCAAGAAGTATCTTAAATCTAAATCTCAAATCACCAAGGACTATGTTTGTCCAATT	2158
Db	121	TCAAGAAGTATCTTAAATCTAAATCTCAAATCACCAAGGACTATGTTTGTCCAATT	180
Qy	2159	GTGGACCAACTTGAGCCTGTATCCATTCTCTAACCAATAAAAAAGAAAAGAGATC	2218
Db	181	GTGGACCAACTTGAGCCTGTATCCATTCTCTAACCAATAAAAAGAAAAGAGATC	240
Qy	2219	AATTGATAAATTCTCAGCCACAAATTCTACATTAGGTTTAGCATATCGAAGGCTCA	2278
Db	241	AATTGATAAATTCTCAGCCACAAATTCTACATTAGGTTTAGCATATCGAAGGCTCA	300
Qy	2279	ATCACAAATACAATAGATAGACTAGAGATTCCAGCGTCACGTGAGTTTATCTATAAATA	2338
Db	301	ATCACAAATACAATAGATAGACTAGAGATTCCAGCGTCACGTGAGTTTATCTATAAATA	360
Qy	2339	AAGGCCAAAAATCAAATCCGAGGCCATTCTGTAATCTAACATAAAACCTTAAACTT	2398
Db	361	AAGGCCAAAAATCAAATCCGAGGCCATTCTGTAATCTAACATAAAACCTTAAACTT	420
Qy	2399	CAAGTCTCATTTAAACAAATCATGTTCACAAAGTCTCTCTCTCTGTTCTCAT	2458
Db	421	CAAGTCTCATTTAAACAAATCATGTTCACAAAGTCTCTCTCTCTGTTCTCAT	480
Qy	2459	CTCTTGCTCATTTCTCTCTGAAACCATGGGGGGCAACAAACACACACACATCTTC	2518
Db	481	CTCTTGCTCATTTCTCTCTGAAACCATGGGGGGCAACAAACACACACACATCTTC	540
Qy	2519	TTCGATCTCTTCTCCACAAACCATCTCTCTCTCCAAATCACCATTAACCATCTC	2578
Db	541	TTCGATCTCTTCTCCACAAACCATCTCTCTCTCCAAATCACCATTAACCATCTC	600
Qy	2579	CAGATTCTCCCTCCATTCTCCCTAACCCCCAACAAATCATCTCTCTCTCCGCCCG	2638
Db	601	CAGATTCTCCCTCCATTCTCCCTAACCCCCAACAAATCATCTCTCTCTCCGCCCG	660
Qy	2639	CGGTATCAAATCCAGCTCTCCCTCCATCTCCGGGTGCTAACACAAACCAATGT	2698
Db	661	CGGTATCAAATCCAGCTCTCCCTCCATCTCCGGGTGCTAACACAAACCAATGT	720
Qy	2699	CACAACCCTCCCTCCACCAACCAACCTACCAACCCGAACATTATCTCCGATTGCG	2758
Db	721	CACAACCCTCCCTCCACCAACCAACCTACCAACCCGAACATTATCTCCGATTGCG	780
Qy	2759	TCCAGATCAACCCCGAACGGGCGTGATATCTCTCGTCAAGCTTAAACGTCAGGCGT	2818
Db	781	TCCAGATCAACCCCGAACGGGCGTGATATCTCTCGTCAAGCTTAAACGTCAGGCGT	840
Qy	2819	AGAAACCGTATTGCGTTACCTGGAGGTGCATCAATGGAGATTACCAAGCCTAACCCG	2878
Db	841	AGAAACCGTATTGCGTTACCTGGAGGTGCATCAATGGAGATTACCAAGCCTAACCCG	900

Qy	2879	CTCTTCCTCAATCGTAACGTCCTTCCTCGTCACGAACAAGGAGGTGTTAGTCAGCAGAGA	2938
Db	901	CTCTTCCTCAATCGTAACGTCCTTCCTCGTCACGAACAAGGAGGTGTTAGTCAGCAGAGA	960
Qy	2939	AGGATACGCTCGATCCTCAGGTAAACCAGGTATCTGTATAGCCACTTCAGGTCCGGAGC	2998
Db	961	AGGATACGCTCGATCCTCAGGTAAACCAGGTATCTGTATAGCCACTTCAGGTCCGGAGC	1020
Qy	2999	TACAAATCTCGTTAGCGGATTAGCCGATGCGTTAGTAGATAGTGTCCCTCTGTAGCAAT	3058
Db	1021	TACAAATCTCGTTAGCGGATTAGCCGATGCGTTAGTAGATAGTGTCCCTCTGTAGCAAT	1080
Qy	3059	CACAGGACAAGCTCCTCGTCGATGATTGGTACAGATGCGTTCAAGAGACTCCGATTGT	3118
Db	1081	CACAGGACAAGCTCCTCGTCGATGATTGGTACAGATGCGTTCAAGAGACTCCGATTGT	1140
Qy	3119	TGAGGTTAACCGCTTCGATTACCGAACGATTAACATCTGTGATGGATGTTGAAGATATCCC	3178
Db	1141	TGAGGTTAACCGCTTCGATTACCGAACGATTAACATCTGTGATGGATGTTGAAGATATCCC	1200
Qy	3179	TAGGATTATTGAGGAAGCTTCTTTAGCTACTCTGGTAGACCTGGACCTGTTGGT	3238
Db	1201	TAGGATTATTGAGGAAGCTTCTTTAGCTACTCTGGTAGACCTGGACCTGTTGGT	1260
Qy	3239	TGATGTTCTAAAGATATTCAACAACAGCTGCGATTCCTAATTGGAACAGGCTATGAG	3298
Db	1261	TGATGTTCTAAAGATATTCAACAACAGCTGCGATTCCTAATTGGAACAGGCTATGAG	1320
Qy	3299	ATTACCTGGTTATATGCTAGGATGCTAAACCTCCGAAGATTCTCATTGGAGCAGAT	3358
Db	1321	ATTACCTGGTTATATGCTAGGATGCTAAACCTCCGAAGATTCTCATTGGAGCAGAT	1380
Qy	3359	TGTTAGGTTGATTCTGAGCTAAGAAGCCTGTTGTTAGTGTGGTGGTGGTTGAA	3418
Db	1381	TGTTAGGTTGATTCTGAGCTAAGAAGCCTGTTGTTAGTGTGGTGGTGGTTGAA	1440
Qy	3419	TTCTACGCGATGATTGGTAGGTTGTTGAGCTAACGGGATCCCTGTTGCGAGTACGTT	3478
Db	1441	TTCTACGCGATGATTGGTAGGTTGTTGAGCTAACGGGATCCCTGTTGCGAGTACGTT	1500
Qy	3479	GATGGGGCTGGGATCTTATCCTGTGATGATGAGTTGTCGTTACATATGCTTGAATGCA	3538
Db	1501	GATGGGGCTGGGATCTTATCCTGTGATGATGAGTTGTCGTTACATATGCTTGAATGCA	1560
Qy	3539	TGGGACTGTGATGCAAAATTACGCTGTTGAGCATAGTGAATTGTTGTCGTTGGGGT	3598
Db	1561	TGGGACTGTGATGCAAAATTACGCTGTTGAGCATAGTGAATTGTTGTCGTTGGGGT	1620
Qy	3599	AAGGTTTGATGATCGTCACGGGTAAGCTGAGGCTTTGCTAGTAGGGCTAAGATTGT	3658
Db	1621	AAGGTTTGATGATCGTCACGGGTAAGCTGAGGCTTTGCTAGTAGGGCTAAGATTGT	1680
Qy	3659	TCATATTGATATTGACTCGCGTAGGATTGGGAAAGAATAAGACTCCTCATGTCGTTGT	3718
Db	1681	TCATATTGATATTGACTCGCGTAGGATTGGGAAAGAATAAGACTCCTCATGTCGTTGT	1740
Qy	3719	TGGTATGTTAACGCTGGCTTGCAGGGATGAATAAGGTTCTGAGAACCGAGCGAGGA	3778
Db	1741	TGGTATGTTAACGCTGGCTTGCAGGGATGAATAAGGTTCTGAGAACCGAGCGAGGA	1800
Qy	3779	GCTTAAGCTTGGATTGGAGGATGAGTTGGAACGTACAGAACAGAACAGTTCC	3838

Db	1801	GCTTAAGCTTGATTTGGAGTTGGAGGAATGAGTTCAGCTACAGAAACAGAAAGTTCC	1860
Qy	3839	GTTGAGCTTAAGCGTTGGGGAAAGCTATCCCTCACAGTATGCGATTAAGGTCCTTGA	3898
Db	1861	GTTGAGCTTAAGCGTTGGGGAAAGCTATCCCTCACAGTATGCGATTAAGGTCCTTGA	1920
Qy	3899	TGAGTTGACTGATGGAAAAGCCATAATAAGTACTGGTGTGGCAACATCAAATGTGGC	3958
Db	1921	TGAGTTGACTGATGGAAAAGCCATAATAAGTACTGGTGTGGCAACATCAAATGTGGC	1980
Qy	3959	GGCGCAGTCTACAAATTACAAGAACCAAGGCAGTGGCTATCATCAGGAGGCCTGGAGC	4018
Db	1981	GGCGCAGTCTACAAATTACAAGAACCAAGGCAGTGGCTATCATCAGGAGGCCTGGAGC	2040
Qy	4019	TATGGGATTGGACTTCTGCTCGATTGGAGCGCTCTGGCTAACCTGTGCGATAGT	4078
Db	2041	TATGGGATTGGACTTCTGCTCGATTGGAGCGCTCTGGCTAACCTGTGCGATAGT	2100
Qy	4079	TGTGGATATTGACGGAGATGGAAGCTTATAATGAATGTGCAAGAGCTAGCCACTATCG	4138
Db	2101	TGTGGATATTGACGGAGATGGAAGCTTATAATGAATGTGCAAGAGCTAGCCACTATCG	2160
Qy	4139	TGTAGAGAATCTCCAGTGAAGGTACTTTATAAACAAACCGCATCTGGCATGGTT	4198
Db	2161	TGTAGAGAATCTCCAGTGAAGGTACTTTATAAACAAACCGCATCTGGCATGGTT	2220
Qy	4199	GCAATGGGAAGATCGGTTCTACAAAGCTAACCGAGCTCACACATTCTCGGGGATCCGC	4258
Db	2221	GCAATGGGAAGATCGGTTCTACAAAGCTAACCGAGCTCACACATTCTCGGGGATCCGC	2280
Qy	4259	TCAGGAGGACGAGATATCCCGAACATGTTGCTTTGCAGCAGCTTGGGGATTCAGC	4318
Db	2281	TCAGGAGGACGAGATATCCCGAACATGTTGCTTTGCAGCAGCTTGGGGATTCAGC	2340
Qy	4319	GGCAGGGGTGACAAAGAACAGATCTCGAGAAGCTATTAGACAATGCTGGATACACC	4378
Db	2341	GGCAGGGGTGACAAAGAACAGATCTCGAGAAGCTATTAGACAATGCTGGATACACC	2400
Qy	4379	AGGACCTTACCTGTTGGATGTGATTGTCGCCACCAAGAACATGTTGCGGATGATCCC	4438
Db	2401	AGGACCTTACCTGTTGGATGTGATTGTCGCCACCAAGAACATGTTGCGGATGATCCC	2460
Qy	4439	GAATGGTGGCATTCAACCGATGTCATAACCGGAGGAGATGGCCGATTAAATACTGAGA	4498
Db	2461	GAGTGGTGGCATTCAACCGATGTCATAACCGGAGGAGATGGCCGATTAAATACTGAGA	2520
Qy	4499	GATGAAACCGGTGATTATCAGAACCTTTATGGCTTGTATGCTATGGAAAAAAACT	4558
Db	2521	GATGAAACCGGTGATTATCAGAACCTTTATGGCTTGTATGCTATGGAAAAAAACT	2580
Qy	4559	TAGTTTGCATTCCTGTTGGTAATTGAGTTCTTTAGTTGATCTGCCT	4618
Db	2581	TAGTTTGCATTCCTGTTGGTAATTGAGTTCTTTAGTTGATCTGCCT	2640
Qy	4619	GCTTTTGGTTACGTCAAGACTACTGCTGTTGGTTGGTTCTTCTTCTTCAATT	4678
Db	2641	GCTTTTGGTTACGTCAAGACTACTGCTGTTGGTTGGTTCTTCTTCAATT	2700
Qy	4679	TATAAATAAATAATCCGGTTCGGTTACTCCTTGTGACTGGCTCAGTTGGTATTGCGA	4738

Db 2701 TATAAATAAATAATCCGGTCCGGTTACTCCTGTGACTGGCTCAGTTGGTTATTGCGA 2760
Qy 4739 AATGCGAATGGTAAATTGAGTAATTGAAATTCGTTATTAGGGTCTAAGCTGTTAAC 4798
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2761 AATGCGAATGGTAAATTGAGTAATTGAAATTCGTTATTAGGGTCTAAGCTGTTAAC 2820
Qy 4799 GTCACTGGGTTAATATCTCTCGAATCTGCATGGAAAATGCTCTTACCATGGTTTAA 4858
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2821 GTCACTGGGTTAATATCTCTCGAATCTGCATGGAAAATGCTCTTACCATGGTTTAA 2880
Qy 4859 TTGAAATGTGCTCATATGGGCCGTGGT 4885
||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2881 TTGAAATGTGCTCATATGGGCCGTGGT 2907
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